

1 **IN THE CLAIMS**

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3 This listing of claims will replace all prior versions, and listings, of claims in the
4 application:

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6 --1. **(Previously Presented)** A method for analyzing a biological sample using a Fourier
7 Transform Mass Spectrometer (FTMS), said method comprising the steps of:

- 8 a. ionizing a drug-dosed biological sample to produce sample (molecular) ions;
9 b. introducing said ions into an analysis region of said FTMS;
10 c. analyzing said ions to determine the molecular weight and abundance of said ions;
11 d. utilizing said molecular weight to determine the empirical formula of each species
12 of said sample; and
13 e. identifying each said species by comparing said empirical formula to a database
14 of formulas for known molecules.

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16 2. **(Original)** A method according to claim 1, wherein said determining of the molecular weight
17 is performed with an accuracy sufficient to identify empirical formula of said ions.

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19 3. **(Previously Presented)** A method according to claim 1, wherein said database of known
20 molecules is updated with said determined empirical formulas.

1 **4. (Previously Presented)** A method for analyzing a biological sample using a Fourier
2 Transform Mass Spectrometer (FTMS), said method comprising the steps of:

- 3 a. ionizing a drug-dosed biological sample to produce sample (molecular) ions;
- 4 b. introducing said ions into an analysis region of said FTMS;
- 5 c. analyzing said ions to determine the molecular weight and abundance of said ions;
- 6 d. determining the molecular structure of each species by multiple stages of mass
7 spectrometry; and
- 8 e. producing a profile of the sample showing structure and concentration data for
9 each species.

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11 **5. (Original)** A method according to claim 4, wherein said determining of the molecular weight
12 is performed with an accuracy sufficient to identify empirical formula of said ions.

1 **6. (Previously Presented)** A method for analyzing a biological sample using a Fourier
2 Transform Mass Spectrometer (FTMS), said method comprising the steps of:

- 3 a. ionizing a drug-dosed biological sample to produce sample precursor ions;
- 4 b. introducing said ions into the analysis region of said FTMS;
- 5 c. analyzing said ions to determine the molecular weight, the abundance and the
6 empirical formula of said ions;
- 7 d. fragmenting said sample precursor ions to produce fragment ions;
- 8 e. determining the molecular weight, the abundance and empirical formula of said
9 fragment ions;
- 10 f. determining the structure of said fragment ions by comparing said empirical
11 formulas of said fragment ions to a database of fragments with known structure;
- 12 g. combining said structures of said fragment ions to determine the precursor ion
13 structure for each species in said sample; and
- 14 h. producing a profile of said sample showing structure and concentration data for
15 selected species of said sample.

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17 **7. (Original)** A method according to claim 6, wherein said determining of the molecular weight
18 is performed with an accuracy sufficient to identify empirical formula of said ions.

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20 **8. (Original)** A method according to claim 6, wherein said fragmenting is performed using
21 photodissociation.

1 **9. (Previously Presented)** A method for analyzing a biological sample utilizing Fourier

2 Transform Mass Spectrometry (FTMS), said method comprising the steps of:

3 a. ionizing polar molecules from a drug-dosed biological sample using positive and
4 negative electrospray to produce sample (molecular) ions;

5 b. introducing said ions into an analysis region of said FTMS;

6 c. analyzing said ions to determine the molecular weight and abundance of said ions;

7 d. utilizing said molecular weight to determine the empirical formula of each species
8 of said sample; and

9 e. identifying each said species by comparing said empirical formula to a database
10 of formulas for known molecules.

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12 **10. (Original)** A method according to claim 9, wherein said determining of the molecular weight
13 is performed with an accuracy sufficient to identify empirical formula of said ions.

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15 **11. (Previously Presented)** A method according to claim 9, wherein said database of known
16 molecules is updated with said determined empirical formulas.

1 **12. (Currently Amended)** A method for analyzing a biological sample utilizing Fourier
2 Transform Mass Spectrometry (FTMS), said method comprising the steps of:

- 3 a. ionizing non-polar molecules from a drug-dosed biological sample using positive
4 and negative ion atmospheric pressure chemical ionization to produce sample (molecular)
5 ions[.];
6 b. introducing said ions into an analysis region of said FTMS;
7 c. analyzing said ions to determine the molecular weight and abundance of said ions;
8 d. utilizing said molecular weight to determine the empirical formula of each species
9 of said sample; and
10 e. identifying each said species by comparing said empirical formula to a database
11 of formulas for known molecules.

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13 **13. (Original)** A method according to claim 12, wherein said determining of the molecular
14 weight is performed with an accuracy sufficient to identify empirical formula of said ions.

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16 **14. (Previously Presented)** A method according to claim 12, wherein said database of known
17 molecules is updated with said determined empirical formulas.

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19 **15. (Previously Presented)** A method according to claim 1, wherein said a drug is injected into
20 said biological sample to create said drug-dosed biological sample.

1 16. **(Previously Presented)** A method according to claim 1, wherein metabolic products are
2 detected.

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4 17. **(Previously Presented)** A method according to claim 1, wherein cellular changes of said
5 drug-dosed biological sample are identified.

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7 18. **(Previously Presented)** A method according to claim 4, wherein said a drug is injected into
8 said biological sample to create said drug-dosed biological sample.

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10 19. **(Previously Presented)** A method according to claim 4, wherein metabolic products are
11 detected.

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13 20. **(Previously Presented)** A method according to claim 4, wherein cellular changes of said
14 drug-dosed biological sample are identified.

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16 21. **(Previously Presented)** A method according to claim 6, wherein said a drug is injected into
17 said biological sample to create said drug-dosed biological sample.

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19 22. **(Previously Presented)** A method according to claim 6, wherein metabolic products are
20 detected.

1 23. **(Previously Presented)** A method according to claim 6, wherein cellular changes of said
2 drug-dosed biological sample are identified.

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4 24. **(Previously Presented)** A method according to claim 9, wherein said a drug is injected into
5 said biological sample to create said drug-dosed biological sample.

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7 25. **(Previously Presented)** A method according to claim 9, wherein metabolic products are
8 detected.

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10 26. **(Previously Presented)** A method according to claim 9, wherein cellular changes of said
11 drug-dosed biological sample are identified.

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13 27. **(Previously Presented)** A method according to claim 12, wherein said a drug is injected into
14 said biological sample to create said drug-dosed biological sample.

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16 28. **(Previously Presented)** A method according to claim 12, wherein metabolic products are
17 detected.

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19 29. **(Previously Presented)** A method according to claim 12, wherein cellular changes of said
20 drug-dosed biological sample are identified.--